

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims

Claims 1-8 (Canceled).

9. (Previously presented) A recombinant enzyme capable of hydrolyzing at least one organophosphate selected from the group consisting of carboxylester organophosphates and dimethyl-oxon organophosphates, wherein the recombinant enzyme comprises an amino acid sequence which is at least about 75% identical to SEQ ID NO.8, wherein the recombinant enzyme comprises amino acid residues conserved between the sequences provided in Figure 4 with the exception that the recombinant enzyme comprises an amino acid selected from the group consisting of Leu, Ser, Ala, Ile, Val, Thr, Cys, Met and Gly at position 251.

10. (Currently amended) A method of eliminating or reducing the concentration of organophosphate pesticide residues in a contaminated sample or substance in which the organophosphate is selected from the group consisting of carboxylester organophosphates and dimethyl-oxon organophosphates, the method comprising contacting the sample or substance with an recombinant enzyme encoded by a DNA molecule comprising an amino acid nucleotide sequence having which is at least 60% homology with Leu E7 identical to SEQ ID NO. 8, in which the protein encoded by the DNA molecule differs from E3 at least in the substitution of Trp at position 251 with wherein the recombinant enzyme comprises amino acid residues conserved between the sequences provided in Figure 4 with the exception that the recombinant enzyme comprises an amino acid selected from the group consisting of Leu, Ser, Ala, Ile, Val, Thr, Cys, Met and Gly at position 251.

11. (Currently amended) A method of eliminating or reducing the concentration of organophosphate pesticide residues in a contaminated sample or substance in which the organophosphate is selected from the group consisting of carboxylester organophosphates and dimethyl-oxon organophosphates, the method comprising contacting the sample or substance with a cell transformed with a DNA molecule encoding a recombinant enzyme comprising an amino acid sequence having which is at least 60% homology with LeuE7 identical to SEQ ID NO. 8, in which the protein encoded by the DNA molecule differs from E3 at least in the substitution of Trp at position 251 with wherein the recombinant enzyme comprises amino acid residues conserved between the sequences provided in Figure 4 with the exception that the recombinant enzyme comprises an amino acid selected from the group consisting of Leu, Ser, Ala, Ile, Val, Thr, Cys, Met and Gly at position 251.

Claims 12 and 13 (Canceled)

14. (Currently amended) The recombinant enzyme according to claim 9, wherein the ~~DNA molecule encoding the recombinant enzyme~~ has at least 80% homology identity with SEQ ID NO. 78

15. (Currently amended) The recombinant enzyme according to claim 9, wherein the ~~DNA molecule encoding the recombinant enzyme~~ has at least 95% homology identity with SEQ ID NO. 78.

16. (Currently amended) The recombinant enzyme according to claim 9, wherein the ~~DNA molecule encoding the recombinant enzyme has~~ is encoded by a DNA molecule comprising the nucleotide sequence of SEQ ID NO:1, 3, or 5, or a sequence which hybridizes under high stringency conditions to SEQ ID NO. 1, 3 or 5, with the proviso that the recombinant enzyme encoded by the DNA molecule differs from SEQ ID NO. 8 at least in the substitution of Trp at position 251 with an amino acid selected from the group consisting of Leu, Ser, Ala, Ile, Val, Thr, Cys, Met and Gly.

17. (Previously presented) The recombinant enzyme according to claim 9, wherein said Trp at position 251 is substituted with Leu or Ser.

18. (Previously presented) A recombinant enzyme capable of hydrolyzing at least one organophosphate selected from the group consisting of carboxylester organophosphates and dimethyl-oxon organophosphates, wherein the recombinant enzyme has the amino acid sequence of SEQ ID NO.10 or the amino acid sequence of SEQ ID NO. 13 in which Trp at position 251 is replaced with Ser.

19. (Currently amended) The method according to claim 10, wherein the recombinant enzyme said DNA molecule has at least 80% ~~homology with the DNA encoding LeuE7~~ identity to SEQ ID NO. 8.

20. (Currently amended) The method according to claim 10, wherein ~~said DNA molecule~~the recombinant enzyme has at least 95% ~~homology with the DNA encoding~~Leu~~E7~~identity to SEQ ID NO. 8.

21. (Currently amended) The method according to claim 10, wherein ~~said the recombinant enzyme is encoded by a DNA molecule~~has comprising the nucleotide sequence of SEQ ID NO:1, 3, or 5, or a sequence which hybridizes under high stringency conditions to SEQ ID NO. 1, 3 or 5, ~~thereto~~ with the proviso that the ~~protein~~recombinant enzyme encoded by the DNA molecule differs from ~~E3~~SEQ ID NO. 8 at least in the substitution of Trp at position 251 with an amino acid selected from the group consisting of Leu, Ser, Ala, Ile, Val, Thr, Cys, Met and Gly.

22. (Original) The method according to claim 10, wherein said Trp at position 251 is substituted with Leu or Ser.

23. (Currently amended) A method of eliminating or reducing the concentration of organophosphate pesticide residues in a contaminated sample or substance in which the organophosphate is selected from the group consisting of carboxylester organophosphates and dimethyl-oxon organophosphates, the method comprising contacting the sample or substance with an recombinant enzyme encoded by a DNA molecule encoding a polypeptide having comprising the amino acid sequence of ~~RM-8~~Con shown in Fig. 1 or the amino acid sequence of ~~Mde~~E7 shown in Fig. 3SEQ ID NO. 10 or SEQ ID NO. 13 in which Trp at position 251 is replaced with Ser.

24. (Original) The method according to claim 11, wherein said cell is a prokaryotic cell or an insect cell.

25. (Currently amended) The method according to claim 11, wherein ~~said DNA molecule~~the recombinant enzyme has at least 80% homology with the DNA encoding ~~LeuE7~~identity to SEQ ID NO. 8.

26. (Currently amended) The method according to claim 11, wherein ~~said DNA molecule~~the recombinant enzyme has at least 95% homology with the DNA encoding ~~LeuE7~~identity to SEQ ID NO. 8.

27. (Currently amended) The method according to claim 11, wherein ~~said the recombinant enzyme is encoded by a DNA molecule~~ has comprising the nucleotide sequence of SEQ ID NO:1, 3, or 5, or a sequence which hybridizes thereto under high stringency conditions to SEQ ID NO. 1, 3 or 5, with the proviso that the ~~protein encoded by the DNA molecule recombinant enzyme~~ differs from ~~E3-SEQ ID NO. 8~~ at least in the substitution of Trp at position 251 with an amino acid selected from the group consisting of Leu, Ser, Ala, Ile, Val, Thr, Cys, Met and Gly.

28. (Original) The method according to claim 11, wherein said Trp at position 251 is substituted with Leu or Ser.

29. (Currently amended) A method of eliminating or reducing the concentration of organophosphate pesticide residues in a contaminated sample or substance in which the organophosphate is selected from the group consisting of carboxylester organophosphates and dimethyl-oxon organophosphates, the method comprising contacting the sample or substance with a cell transformed with a DNA molecule encoding a polypeptiderecombinant enzyme having the amino acid sequence of RM-8C shown in Fig. 4 as provided in SEQ ID NO. 10 or the amino acid sequence of MdxE7 shown in Fig. 3 as provided in SEQ ID NO. 13 in which Trp at position 251 is replaced with Ser.

30. (Previously presented) A recombinant enzyme capable of hydrolyzing at least one organophosphate selected from the group consisting of carboxylester organophosphates and dimethyl-oxon organophosphates, wherein the recombinant enzyme comprises an amino acid sequence which is at least about 60% identical to SEQ ID NO.8, wherein the recombinant enzyme comprises amino acid residues conserved between the sequences provided in Figure 4 with the exception that the recombinant enzyme comprises an amino acid selected from the group consisting of Leu, Ser, Ala, Ile, Val, Thr, Cys, Met and Gly at position 251